SEQUENCE LISTING

<110> KIRIN BEER KABUSHIKI KAISHA
National Institute of Advanced Industrial Science and Technology

<120> A methylotrophic yeast capable of producing a mammalian type sugar chain

<130> PH-1796-PCT

<150> JP 2002-127677
<151> 2002-04-26

<160> 120

<170> PatentIn Ver. 2.0

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<213> Saccharomyces cerevisiae

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer PGP5 for amplification of 5'-region of Ogataea minuta GAP gene

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gcntayatgt tyaartayga ywsnacncay gg 32

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<211> 32

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer PGP3 for amplification of 3'-region of Ogataea minuta GAP gene

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<210> 5

<211> 3186

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 1492..2502

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<212> PRT
<213> Ogataea minuta

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20 25 30

Asn Asp Pro Phe Ile Ala Ala Glu Tyr Ala Ala Tyr Met Phe Lys Tyr
35 40 45

Asp Ser Thr His Gly Arg Tyr Gln Gly Glu Val Thr Phe Glu Gly Lys
50 55 60

Tyr Leu Val Ile Asp Gly Gln Lys Ile Glu Val Phe Gln Glu Arg Asp
65 70 75 80

Pro Ala Asp Ile Pro Trp Gly Lys Glu Gly Val Asp Phe Val Ile Asp
85 90 95

Ser Thr Gly Val Phe Thr Thr Thr Ala Gly Ala Gln Lys His Ile Asp
100 105 110

Ala Gly Ala Lys Lys Val Ile Ile Thr Ala Pro Ser Ala Asp Ala Pro
115 120 125

Met Phe Val Met Gly Val Asn His Lys Glu Tyr Thr Lys Asp Leu Ser
130 135 140

Ile Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala
145 150 155 160

Lys Val Val Asn Asp Val Phe Gly Ile Glu Ser Gly Leu Met Thr Thr
165 170 175

Val His Ser Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser His
180 185 190

Lys Asp Trp Arg Gly Gly Arg Thr Ala Ser Gly Asn Ile Ile Pro Ser
195 200 205

Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Leu Pro Ala Leu Ala
210 215 220

Gly Lys Leu Thr Gly Met Ser Leu Arg Val Pro Thr Thr Asp Val Ser
225 230 235 240

Val Val Asp Leu Thr Val Asn Leu Lys Thr Pro Thr Thr Tyr Ala Glu
245 250 255

Ile Ser Ala Ala Ile Lys Lys Ala Ser Glu Gly Glu Leu Ala Gly Ile
260 265 270

Leu Gly Tyr Thr Glu Asp Ala Val Val Ser Thr Asp Phe Leu Thr Asp
275 280 285

Asn Arg Ser Ser Ile Phe Asp Ala Ser Ala Gly Ile Leu Leu Thr Pro
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Thr Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr Ser
305 310 315 320

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<210> 7
<211> 1491
<212> DNA
<213> Ogataea minuta

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<210> 8

<211> 524

<212> DNA

<213> Ogataea minuta

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<210> 9
<211> 113
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for production of an expression cassette with GAP gene promoter and terminator from Ogataea minuta

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ggatagatga ccaatggcct ctttaagtaa acatttcgtt ttgaatatat ttc 113

<210> 10
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for production of an

expression cassette with GAP gene promoter and terminator from Ogataea minuta

<400> 10

tttttactag tacggtaccg ctcgaatcga cacaggag 38

<210> 11

<211> 12

<212> PRT

<213> Saccharomyces cerevisiae

)

<400> 11

Gly Pro Tyr Ile Cys Leu Val Lys Thr His Ile Asp

1 5 10

<210> 12

<211> 11

<212> PRT

<213> Saccharomyces cerevisiae

)

<400> 12

Gly Arg Gly Leu Phe Gly Lys Gly Arg Asp Pro

1 5 10

<210> 13

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PUR5 for amplification of 5'-region of Ogataea Minuta URA3 gene

<400> 13

ggnccntaya thtgyytngt naaracncay athga 35

<210> 14

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PUR3 for amplification of 3'-region of Ogataea Minuta URA3 gene

<400> 14

ggrtcnckne cyttnccraa narnccnckn cc 32

<210> 15

<211> 3113

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 1732..2529

<400> 15

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<211> 265

<212> PRT

<213> Ogataea minuta

<400> 16

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Leu Cys Ala Ser Val Asp Leu Thr Ser Thr Lys Asp Leu Leu Glu Leu
35 40 45

Leu Asp Lys Leu Gly Pro Phe Ile Cys Leu Val Lys Thr His Ile Asp
50 55 60

Ile Val Glu Asp Phe Ser Tyr Glu Asn Thr Val Val Pro Leu Leu Lys
65 70 75 80

Leu Ala Lys Lys His Asn Phe Met Ile Phe Glu Asp Arg Lys Phe Ala
85 90 95

Asp Ile Gly Asn Thr Val Lys Leu Gln Tyr Lys Gly Gly Val Tyr Gln
100 105 110

Ile Ala Lys Trp Ala Asp Ile Thr Asn Ala His Gly Val Thr Gly Ser
115 120 125

Arg Ile Val Ser Gly Leu Arg Gln Ala Ala Gln Glu Thr Thr Asp Glu
130 135 140

Pro Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Ser Glu Gly Ser Leu
145 150 155 160

Ala Tyr Gly Glu Tyr Thr Lys Lys Thr Val Glu Ile Ala Lys Ser Asp
165 170 175

Arg Asp Phe Val Ile Gly Phe Ile Ala Gln Asn Asp Met Gly Gly Arg
180 185 190

Asp Glu Gly Phe Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp
195 200 205

Asp Thr Gly Asp Ala Leu Gly Gln Gln Tyr Arg Thr Val Ser Ala Val
210 215 220

Met Lys Thr Gly Thr Asp Ile Ile Ile Val Gly Arg Gly Leu Phe Gly
225 230 235 240

Lys Gly Arg Asp Pro Val Val Glu Gly Glu Arg Tyr Arg Lys Ala Gly
245 250 255

Trp Asp Ala Tyr Leu Ser Arg Val Ala
260 265

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for amplification of a gene

fragment conferring resistance against chloramphenicol

<400> 17

atggagaaaa aaactagtgg atataccacc 30

<210> 18

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of a gene fragment conferring resistance against chloramphenicol

<400> 18

ctgagacgaa aaagatatct caataaaccc 30

<210> 19

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DU5 used for confirmation of destruction of Ogataea minuta URA3 gene

<400> 19

aggaagaaga ggaggaagag gaagaaac 28

<210> 20

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DUC5 used for confirmation of destruction of Ogataea minuta URA3 gene

<400> 20

cgatgccatt gggatatatc aacggtgg 28

<210> 21

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DU3 used for confirmation of destruction of Ogataea minuta URA3 gene

<400> 21

ccgtgtttga gtttgtgaaa aaccagggc 29

<210> 22

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DUC3 used for confirmation of destruction of Ogataea minuta URA3 gene

<400> 22

tgtggcgtgt tacggtgaaa acctggcc 28

<210> 23

<211> 14

<212> PRT

<213> Saccharomyces cerevisiae

<400> 23

Phe Val Ala Thr Asp Arg Ile Ser Ala Tyr Asp Val Ile Met
1 5 10

<210> 24

<211> 14

<212> PRT

<213> Saccharomyces cerevisiae

<400> 24

Gln Asp Ser Tyr Asp Lys Gln Phe Leu Arg Asp Trp Leu Thr
1 5 10

<210> 25

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PAD5 for amplification of 5'-region of Ogataea minuta ADE1 gene

<400> 25

ttygtngcna cngaymgnat hwsngcntay gaygtnatha tg 42

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PAD3 for amplification of 3'-region of Ogataea minuta ADE1 gene

<400> 26

gtnarccart cncknarraa ytgyttrtcr tanswrtcyt g 41

<210> 27

<211> 2560

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 939..1850

<400> 27

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caagaacttt tccagtccac tccagagatt gcaccccggg 2560

<210> 28
<211> 303
<212> PRT
<213> Ogataea minuta

<400> 28

Met Ser Leu Thr Thr Thr Asn Leu Asp Gly Ile Leu Pro Leu Ile Ala
1 5 10 15

Lys Gly Lys Val Arg Asp Ile Tyr Gln Val Asp Glu Glu Ser Leu Leu
20 25 30

Phe Val Ala Thr Asp Arg Ile Ser Ala Tyr Asp Val Ile Met Glu Asn
35 40 45

Gly Ile Lys Asp Lys Gly Lys Ile Leu Thr Gln Leu Ser Val Phe Trp
50 55 60

Phe Asp Leu Leu Lys Asp Thr Ile Lys Asn His Leu Ile Ala Ser Thr
65 70 75 80

Asp Asp Glu Val Phe Ala Arg Leu Pro Gln Glu Leu Ser Gln Pro Lys
85 90 95

Tyr Lys Ser Gln Leu Ser Gly Arg Ala Leu Val Val Arg Lys His Lys
100 105 110

Leu Ile Pro Leu Glu Val Ile Val Arg Gly Tyr Ile Thr Gly Ser Ala
115 120 125

Trp Lys Glu Tyr Asn Lys Ser Lys Thr Val His Gly Leu Glu Val Gly
130 135 140

Ala Glu Leu Lys Glu Ser Gln Glu Phe Pro Val Pro Ile Phe Thr Pro
145 150 155 160

Ser Thr Lys Ala Glu Gln Gly Glu His Asp Glu Asn Ile Ser Pro Glu
165 170 175

Lys Ala Ala Glu Ile Val Gly Glu Gln Leu Cys Ala Arg Leu Ala Glu
180 185 190

Lys Ala Val Gln Leu Tyr Ser Lys Ala Arg Thr Tyr Ala Lys Ser Lys
195 200 205

Gly Ile Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asn
210 215 220

Asp Glu Leu Val Leu Val Asp Glu Val Leu Thr Pro Asp Ser Ser Arg
225 230 235 240

Phe Trp Asp Ala Lys Thr Tyr Lys Ile Gly Gln Ser Gln Asp Ser Tyr
245 250 255

Asp Lys Gln Phe Leu Arg Asp Trp Leu Thr Ser Asn Gly Leu Asn Gly
260 265 270

Lys Asp Gly Val Ser Met Thr Ala Glu Ile Ala Glu Arg Thr Gly Ala
275 280 285

Lys Tyr Val Glu Ala Phe Glu Ser Leu Thr Gly Arg Lys Trp Thr
290 295 300

<210> 29
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5'-primer for amplification of

upstream region of URA3 structural gene

<400> 29

ccccgagctc aaaaaaaagg taccaatttc agctccgacg ccggagccca ctacgcctac 60

<210> 30

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 3'-primer for amplification of upstream region of URA3 structural gene

<400> 30

gggaagcttc cccagttgta caccaatctt gtcgacag 38

<210> 31

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Dad1-5 used for destruction of Ogataea minuta ADE1 gene

<400> 31

aaaaagcggc cgctcccggt gtcccgcaga aatctttatg cgtagtcttg 50

<210> 32

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Dad1-3 used for destruction of Ogataea minuta ADE1 gene

<400> 32

cccccggatc cttttttta agcttgttgt actccttcca tgcacttccg gtgatg 56

<210> 33

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Dad2-5 used for destruction of Ogataea minuta ADE1 gene

<400> 33

ttttcacccc gtcaaggatc cctgaacaag gcgaacacga cgaaaacatt tcccccgag 59

<210> 34

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Dad2-3 used for destruction of Ogataea minuta ADE1 gene

<400> 34

tttttgggcc cacctgggtg aagatttgcc agatcaagtt ctcc 44

<210> 35

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DA5 used for confirmation of destruction of Ogataea minuta ADE1 gene

<400> 35

gatgcttgcg ccttcaacca catactcctc 30

<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DA3 used for confirmation of destruction of Ogataea minuta ADE1 gene

<400> 36

aaaagttctt gcacagcctc aatattgacc 30

<210> 37

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DOU5 used for confirmation of destruction of Ogataea minuta ADE1 gene

<400> 37

atcgatttcg agtgtttgtc caggtccggg 30

<210> 38

<211> 10

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> variation

<222> 3

<223> Xaa=His or Arg

<220>

<221> variation

<222> 4

<223> Xaa=Ile or Val

<400> 38

Pro Gln Xaa Xaa Trp Gln Thr Trp Lys Val
1 5 10

<210> 39

<211> 11

<212> PRT

<213> Saccharomyces cerevisiae

<400> 39

Trp Tyr Ala Arg Arg Ile Gln Phe Cys Gln Trp
1 5 10

<210> 40

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer POH5 for amplification of 5'-region of Ogataea minuta OCH1 gene

<400> 40

ccncarcryr thtggcarac ntggaargt 29

<210> 41

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer POH3 for amplification of 3'-region of Ogataea minuta OCH1 gene

<400> 41

ccaytgrcar aaytgdatnc knckngcrta cca 33

<210> 42

<211> 2527

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 508..1812

<400> 42

agatctgttg acactggtca agcgtgtagc caagagaata ggaaacggaa tttcatactg 60

ccggcacaca aggacaataa gggcgtccgg ggctgtcgaa attgtcgaga ccgtagagct 120

attgttacct caataagttg ctctacgatt gtttccgtct ttgacaaagc agtaggcctt 180

tctcaaggtg gtgtacgggt gtttcatttt taatttgcat cgagaacgcg tagtgcgcca 240

atggatctgc agggggctcg gctgattgca ctgaaatttc agcaataaat agctgaggat 300

attcaggcac aacggtacca acggggcagg cttgatcgcg aagcagcagg agaaggcagc 360

gaagtgactg aagagacgag aaggagacga atcagcctac ccctggaacc ataaacaaag 420

tcgagccgtt tttttaggga cagaaaccgt tctggatatt tattcgacgc agagactcgg 480

tagtcatctc tacgttcagc acacaccatg aactatcacg acttgtacga tgatagcaaa 540

cggcagtcgt tgatgcgaaa ggcgcgaaag ttcgctgaga tgaacaagaa gttggtggtg 600

gtggtcattt taacgatgta cgttgtgtcg cgtctggcgt cggttggaag cacgaaacag 660

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tactagt 2527

<210> 43
<211> 434
<212> PRT
<213> Ogataea minuta

<400> 43

Met Asn Tyr His Asp Leu Tyr Asp Asp Ser Lys Arg Gln Ser Leu Met
1 5 10 15

Arg Lys Ala Arg Lys Phe Ala Glu Met Asn Lys Lys Leu Val Val Val
20 25 30

Val Ile Leu Thr Met Tyr Val Val Ser Arg Leu Ala Ser Val Gly Ser
35 40 45

Thr Lys Gln Glu Ser Ile Pro Gly Leu Thr Met Lys Glu Ser Glu Leu
50 55 60

Glu Val Asn Phe Lys Thr Phe Gly Met Asp Leu Gln Lys Arg Asn Glu
65 70 75 80

Leu Pro Ala Ala Ser Ala Thr Leu Arg Glu Lys Leu Ser Phe Tyr Phe
85 90 95

Pro Tyr Asp Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr Trp

100 105 110

Lys Val Asp Ile Asn Asp Lys Ser Phe Pro Arg His Phe Arg Lys Phe
115 120 125

Gln Glu Thr Trp Pro Gln Leu Asn Ser Gly Tyr Thr Tyr His Leu Ile
130 135 140

Pro Asp Ser Ile Val Asp Glu Phe Met Arg Ser Leu Phe Ala Asn Val
145 150 155 160

Pro Glu Val Ile Ala Ala Tyr Asn Met Leu Pro Lys Asn Ile Leu Lys
165 170 175

Ala Asp Phe Phe Arg Tyr Leu Val Ile Phe Ala Arg Gly Gly Thr Tyr
180 185 190

Ser Asp Ile Asp Thr Ile Cys Leu Lys Pro Val Asn Glu Trp Ala Thr
195 200 205

Phe Asn Glu Gln Thr Val Ile Ser His Tyr Leu Lys Thr Asn Gly Lys
210 215 220

Thr Ser Gln Leu Pro Glu Val Asp Pro Ser Thr Arg Lys Thr Pro Ile
225 230 235 240

Gly Leu Thr Ile Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His
245 250 255

Glu Trp Tyr Ala Arg Arg Ile Gln Phe Cys Gln Trp Thr Ile Gln Gly
260 265 270

Lys Gln Gly His Pro Met Leu Arg Glu Leu Ile Ile Arg Ile Val Glu
275 280 285

Gln Thr Phe Arg Lys Glu Ala Met Gly Asn Leu Lys Lys Val Glu Gly
290 295 300

Lys Asp Met Gly Gly Asp Ile Met Gln Trp Thr Gly Pro Gly Val Phe
305 310 315 320

Thr Asp Thr Leu Phe Asp Tyr Leu Asn Asn Val Val Ser Asp Gly Lys
325 330 335

Leu Gly Asp Gly Tyr Gly Val Gly Ser Lys Tyr Trp Asn Ser His Ala
340 345 350

Lys Tyr Lys Leu Ser His Ile Glu Val Asp Ala Asn Asn Glu Pro Met
355 360 365

His Ser Asp Lys Gln Thr Ile Ser Trp Lys Ser Met Ser Lys Leu Ser
370 375 380

Glu Pro Leu Ile Ile Asp Asp Val Met Ile Leu Pro Ile Thr Ser Phe
385 390 395 400

Ser Pro Gly Val Gly Gln Met Gly Ser His Ser Pro Asp His Pro Leu
405 410 415

Ala Phe Val Arg His Met Phe Gln Gly Ser Trp Lys Pro Asp Ala Glu
420 425 430

Lys Met

<210> 44
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D03 used for confirmation of destruction of Ogataea minuta OCH1 gene

<400> 44
ccattgtcag ctccaattct ttgataaacg 30

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer D05 used for confirmation of destruction of Ogataea minuta OCH1 gene

<400> 45

acacttccgt aagttccaag agacatggcc 30

<210> 46

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DO3-2 used for confirmation of destruction of Ogataea minuta OCH1 gene

<400> 46

tcaccacgtt attgagataa tcaaacaggg 30

<210> 47

<211> 8

<212> PRT

<213> Saccharomyces cerevisiae

<400> 47

Thr Asn Tyr Leu Asn Ala Gln Tyr

1 5

<210> 48

<211> 8

<212> PRT

<213> Saccharomyces cerevisiae

<400> 48

Lys Ala Tyr Trp Glu Val Lys Phe
1 5

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer PPA5 for amplification of 5'-region of Ogataea minuta PEP4 gene

<400> 49
acnaaytayy tnaaygcnca rta 23

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer PPA3 for amplification of 3'-region of Ogataea minuta PEP4 gene

<400> 50
aayttnacyt cccartangc ytt 23

<210> 51
<211> 1951

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 477..1709

<400> 51

catatgtatt catcaatcta cagcttttct aatcngtgtg acttcagtca catgatcctc 60
tgacccgcca cgaccttgct ggcttccagc gcgcgaaact cactcccaat tttcggatta 120
gctaatcacg aagatttttg gatttcctga tctgtagtgt atccatcctg ccttaatcgt 180
tttcgataca tttgttatcc gaattgggaa tggcattagt cgtgcgccac ccgactcgcc 240
acccccattc tagtggcaaa caggattgaa agagggctaa aaggtaactt agtgttttat 300
ctctgaatct tccttctgat atcaatcaac aattgttaaa cgattgaaag ttttgaaaca 360
ttcattgaac ttgcgaagcg ctcacacagc atcgttcggt tagcagttac aacagtttag 420
gtttttttcc ccacaaaaag gctcacgctg cctcctcact cttgcctctt ttcttgatga 480
aactctcgct tgcattgctc gcccttggtg gtttccaaga ggcccacgcc aaggttcatc 540
atgcgccaat caagaagact cctgccgcgg aaacttacaa ggacgtgagt ttcggcgact 600
acgtggattc tctgaagggc aagtatgtct ctatgtttgc taagcatgct gcggagtcct 660
cccaaaacgc ctttgtccct tttgttcagg aagtgcaaga cccagagttt actgttcagg 720
agggacacaa ctccccctctc acgaactacg tgaacgctca gtacttcact gagattcaaa 780
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tggtatgttt attgctttta ttacgtgacc aaatgttggt ttttctttca ccttttactc 1860
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tgaattgcac aaatttaaag attgctctag a 1951

<210> 52
<211> 410
<212> PRT
<213> Ogataea minuta

<400> 52
Met Lys Leu Ser Leu Ala Leu Leu Ala Leu Gly Gly Phe Gln Glu Ala
1 5 10 15

His Ala Lys Val His His Ala Pro Ile Lys Lys Thr Pro Ala Ala Glu
20 25 30

Thr Tyr Lys Asp Val Ser Phe Gly Asp Tyr Val Asp Ser Leu Lys Gly
35 40 45

Lys Tyr Val Ser Met Phe Ala Lys His Ala Ala Glu Ser Ser Gln Asn

50 55 60

Ala Phe Val Pro Phe Val Gln Glu Val Gln Asp Pro Glu Phe Thr Val
65 70 75 80

Gln Glu Gly His Asn Ser Pro Leu Thr Asn Tyr Val Asn Ala Gln Tyr
85 90 95

Phe Thr Glu Ile Gln Ile Gly Thr Pro Gly Gln Pro Phe Lys Val Ile
100 105 110

Leu Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Gly Ser Asp Cys Ser
115 120 125

Ser Leu Ala Cys Tyr Leu His Gln Lys Tyr Asp His Asp Ser Ser Ser
130 135 140

Thr Tyr Lys Ala Asn Gly Ser Glu Phe Ala Ile Arg Tyr Gly Ser Gly
145 150 155 160

Ser Leu Glu Gly Phe Val Ser Gln Asp Thr Leu Thr Leu Gly Asp Leu
165 170 175

Ile Ile Pro Lys Gln Asp Phe Ala Glu Ala Thr Ser Glu Pro Gly Leu
180 185 190

Ala Phe Ala Phe Gly Lys Phe Asp Gly Ile Leu Gly Leu Ala Tyr Asp
195 200 205

Thr Ile Ser Val Asp Lys Ile Val Pro Pro Ile Tyr Asn Ala Leu Asn
210 215 220

Leu Gly Leu Leu Asp Glu Pro Gln Phe Ala Phe Tyr Leu Gly Asp Thr
225 230 235 240

Ala Lys Ser Glu Ala Asp Gly Gly Val Ala Thr Phe Gly Gly Val Asp
245 250 255

Glu Thr Lys Tyr Asp Gly Lys Ile Thr Trp Leu Pro Val Arg Arg Lys
260 265 270

Ala Tyr Trp Glu Val Lys Phe Asp Gly Ile Ala Leu Gly Asp Glu Tyr
275 280 285

Ala Thr Leu Asp Gly Tyr Gly Ala Ala Ile Asp Thr Gly Thr Ser Leu
290 295 300

Ile Ala Leu Pro Ser Gln Leu Ala Glu Ile Leu Asn Ser Gln Ile Gly
305 310 315 320

Ala Glu Lys Ser Trp Ser Gly Gln Tyr Thr Ile Asp Cys Glu Lys Arg
325 330 335

Ala Ser Leu Pro Asp Leu Thr Phe Asn Phe Asp Gly Tyr Asn Phe Ser
340 345 350

Ile Ser Ala Tyr Asp Tyr Thr Leu Glu Val Ser Gly Ser Cys Ile Ser
355 360 365

Ala Phe Thr Pro Met Asp Phe Pro Ala Pro Ile Gly Pro Leu Ala Ile
370 375 380

Ile Gly Asp Ala Phe Leu Arg Lys Tyr Tyr Ser Val Tyr Asp Leu Gly
385 390 395 400

Lys Asp Ala Val Gly Leu Ala Lys Ala Val
405 410

<210> 53
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> variation
<222> 2
<223> Xaa=Gly or Leu

<400> 53
Asp Xaa Asn Gly His Gly Thr His Cys Ala Gly
1 5 10

<210> 54
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<220>

<221> variation

<222> 6

<223> Xaa=Ser or Thr

<220>

<221> variation

<222> 9

<223> Xaa=Val or Ile

<220>

<221> variation

<222> 10

<223> Xaa=Ala or Val

<400> 54

Gly Thr Ser Met Ala Xaa Pro His Xaa Xaa Gly
1 5 10

<210> 55

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PPB5 for amplification of 5'-region of Ogataea minuta PRB1 gene

<400> 55

gaybknaayg gncayggnac ncaytgykcn gg 32

<210> 56

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PPB3 for amplification of 3'-region of Ogataea minuta PRB1 gene

<400> 56

ccnrcnayrt gnggnwsngc catnwsngtn cc 32

<210> 57

<211> 2214

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 394..2013

<400> 57

ggatcccctc tctcgctagc gagtttcgcc tgctctgcga taagagaaaa ccggctgtgc 60

agctttcacc ccaacacgtc actttctgca gtcgtgcgcc ggcttgcatt aggtcgtgcg 120

cagatcccaa atttgccacc agactaaatt ggggcattct ggtgagggaa taggggaaat 180

aagagggtgt tttgacgttt catatacatt gctctttctt ttcttggacg gttagcggta 240

ttgccataga ttatcttgcg cagttcagca tccttaggag ttattctttc ttgtaggtct 300

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gtcgccgaag aggttgctga tttgttcgat taggtttcta acaattcagt gatcttgtct 2040

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cgcttttcct ttttttttctg ttgtttggag tgtttgtttt tctggataat gtggttagtt 2160
tttcaagttg cttccaatat tgtttgtcca gattagagtc attgcttgaa gctt 2214

<210> 58
<211> 539
<212> PRT
<213> Ogataea minuta

<400> 58

Met Lys Leu Ser Gln Ser Ala Ala Val Ala Ile Leu Ser Ser Leu Ala
1 5 10 15

Ala Val Glu Ala Leu Val Ile Pro Leu Phe Asp Asp Leu Pro Ala Glu
20 25 30

Phe Ala Leu Val Pro Met Asp Ala Lys Ala Glu Val Ile Ser Asp Val
35 40 45

Pro Val Asp Ser Ala Ile Ser Asp Ala Pro Ile Ala Ala Leu Asn Asp
50 55 60

Ala Pro Ser Pro Leu Val Thr Ser Leu Ile Ala Ser Gln Asn Leu Ile
65 70 75 80

Pro Asn Ser Tyr Ile Val Val Phe Lys Asn Gly Leu Ala Ser Gly Ala
85 90 95

Val Asp Phe His Met Glu Trp Leu Lys Glu Thr His Ser Gln Thr Leu

100 105 110

Ala Ala Leu Ser Lys Asp Met Pro Ala Glu Glu Leu Ala Ala Glu Gly
115 120 125

Phe Val Ser Glu Ser Ile Asp Leu Thr Glu Val Phe Ser Ile Ser Asp
130 135 140

Leu Phe Ser Gly Tyr Thr Gly Tyr Phe Pro Glu Lys Val Val Asp Leu
145 150 155 160

Ile Arg Arg His Pro Asp Val Ala Phe Val Glu Gln Asp Ser Arg Val
165 170 175

Phe Ala Asp Lys Ser Ser Thr Gln Asn Gly Ala Pro Trp Gly Leu Ser
180 185 190

Arg Ile Ser His Arg Glu Pro Leu Ser Leu Gly Asn Phe Asn Glu Tyr
195 200 205

Val Tyr Asp Asp Leu Ala Gly Asp Gly Val Thr Ala Tyr Val Ile Asp
210 215 220

Thr Gly Ile Asn Val Lys His Glu Gln Phe Gly Gly Arg Ala Glu Trp
225 230 235 240

Gly Lys Thr Ile Pro Thr Gly Asp Asp Asp Ile Asp Gly Asn Gly His
245 250 255

Gly Thr His Cys Ala Gly Thr Ile Gly Ser Glu Asp Tyr Gly Val Ser
260 265 270

Lys Asn Ser Lys Ile Val Ala Val Lys Val Leu Arg Ser Asn Gly Ser
275 280 285

Gly Ser Met Ser Asp Val Ile Lys Gly Val Glu Phe Ala Ala Asn Asp
290 295 300

His Val Ala Lys Ser Lys Ala Lys Lys Asp Gly Phe Lys Gly Ser Thr
305 310 315 320

Ala Asn Met Ser Leu Gly Gly Gly Lys Ser Pro Ala Leu Asp Leu Ala
325 330 335

Val Asn Ala Ala Val Lys Ala Gly Leu His Phe Ala Val Ala Ala Gly
340 345 350

Asn Asp Asn Ala Asp Ala Cys Asn Tyr Ser Pro Ala Ala Ala Glu Asn
355 360 365

Ala Val Thr Val Gly Ala Ser Thr Leu Ser Asp Ser Arg Ala Tyr Phe
370 375 380

Ser Asn Tyr Gly Lys Cys Val Asp Ile Phe Ala Pro Gly Leu Asn Ile
385 390 395 400

Leu Ser Thr Tyr Ile Gly Ser Asp Thr Ala Thr Ala Thr Leu Ser Gly
405 410 415

Thr Ser Met Ala Ser Pro His Val Cys Gly Leu Leu Thr Tyr Phe Leu
420 425 430

Ser Leu Gln Pro Glu Ser Ser Ser Leu Phe Ser Ser Ala Ala Ile Ser
435 440 445

Pro Ala Gln Leu Lys Lys Asn Leu Ile Lys Phe Gly Thr Lys Asn Val
450 455 460

Leu Ser Glu Ile Pro Ser Asp Gly Thr Pro Asn Ile Leu Ile Tyr Asn
465 470 475 480

Gly Ala Gly Lys Asn Ile Ser Asp Phe Trp Ala Phe Glu Asp Glu Ala
485 490 495

Ser Ala Lys Ser Asp Leu Lys Lys Ala Val Asp Ile Ala Thr Ser Val
500 505 510

Asp Leu Asp Leu Gln Asp Ile Lys Glu Lys Phe Asn His Ile Leu Glu
515 520 525

Glu Val Ala Glu Glu Val Ala Asp Leu Phe Asp
530 535

<210> 59
<211> 9
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> variation
<222> 1
<223> Xaa=His or Asn

<220>
<221> variation
<222> 5
<223> Xaa=Val or Thr

<400> 59
Xaa Tyr Asp Trp Xaa Phe Leu Asn Asp
1 5

<210> 60
<211> 12
<212> PRT
<213> Saccharomyces cerevisiae

<400> 60
Tyr Asn Leu Cys His Phe Trp Ser Asn Phe Glu Ile
1 5 10

<210> 61
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PKR5 for amplification of 5'-region of Ogataea minuta KTR1 gene

<400> 61

maytaygayt ggrynttyyt naayga 26

<210> 62

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PKR3 for amplification of 3'-region of Ogataea minuta KTR1 gene

<400> 62

atytcraart tnswccaraa rtgrcanarr ttrta 35

<210> 63

<211> 1930

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 124..1335

<400> 63

gagctctata tttagctttg gacattggta ctagttggac tgttgatcgg ttgacttgac 60
agtgagttct atagaaagac aggctacaaa gaccaccaag gctggcaaat ttgcgagatt 120
acaatggcta gagcgaatgc gaggctgatc cggtttgcaa tctttgctac cgtgttggtt 180
ttatgtggat acattttatc caagggctcg tctacttcgt atacgatttc gacgccagag 240
tccggctcga gttccagtgg cactgttgct aatactgaga aatctgccct cgcagtgggt 300
gagaaaagcg ttgcaggcgc agccgagaaa agcgttcctg cagctgacgt cccagatgga 360
aaggtgaagg ccacttttgt ctctttggcc agaaaccagg atctgtggga gctggtgaac 420
tcgatcagac aggtcgaaga ccgtttcaac aacaagtatc attacgattg ggtgttcttg 480
aacgacgcgg aattcaacga cgagttcaag aaggtgacct ctcaggtctg ttcgggtaag 540
accaagtatg gtgtcattcc aaaggaacag tggagcttcc cttcgtggat cgacactgat 600
aaggctgctg ccaccagaga gcaaatgaga aaggacaaga tcatctacgg agactccatc 660
tcgtacagac acatgtgcag atacgagtcg ggattcttct tcaaacaccc agaactcgca 720
gagtacgagt actactggag agtggagcca agcatcaaga tctactgtga cattgactac 780
gacatcttca agttcatgaa ggacaacaag aagtcgtacg gatggaccat ttctcttcct 840
gagtacaagg agaccatccc aactctgtgg aagaccacta gagacttcat gaaggaaaac 900
ccacagtacg ttgcccagga caacctgatc aactttattt cggacgacgg aggaagcagc 960
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gatgagcttc gagaacgttc tcgaggttct agaagactct gcgtctgagt gctccaagaa 1680
caaggacttc ctctccttct cgacgatcat cgacgtccat ctgggtgatc tttccattta 1740

cactgagtcc gagcgacttg agctgttgtc gaaactgaca tctattctga gcaatgacca 1800
ccaattggtt tacgaggtag gatgggactt accaccgatc atattcagct tcctggactc 1860
tgaatcttcg cccagtgagg ggctgatgaa cagcaaggtc acggttcttt tcttgaagct 1920
gtttgagctc 1930

<210> 64
<211> 403
<212> PRT
<213> Ogataea minuta

<400> 64

Met Ala Arg Ala Asn Ala Arg Leu Ile Arg Phe Ala Ile Phe Ala Thr
1 5 10 15

Val Leu Val Leu Cys Gly Tyr Ile Leu Ser Lys Gly Ser Ser Thr Ser
20 25 30

Tyr Thr Ile Ser Thr Pro Glu Ser Gly Ser Ser Ser Ser Gly Thr Val
35 40 45

Ala Asn Thr Glu Lys Ser Ala Leu Ala Val Gly Glu Lys Ser Val Ala
50 55 60

Gly Ala Ala Glu Lys Ser Val Pro Ala Ala Asp Val Pro Asp Gly Lys
65 70 75 80

Val Lys Ala Thr Phe Val Ser Leu Ala Arg Asn Gln Asp Leu Trp Glu
85 90 95

Leu Val Asn Ser Ile Arg Gln Val Glu Asp Arg Phe Asn Asn Lys Tyr
100 105 110

His Tyr Asp Trp Val Phe Leu Asn Asp Ala Glu Phe Asn Asp Glu Phe
115 120 125

Lys Lys Val Thr Ser Gln Val Cys Ser Gly Lys Thr Lys Tyr Gly Val
130 135 140

Ile Pro Lys Glu Gln Trp Ser Phe Pro Ser Trp Ile Asp Thr Asp Lys
145 150 155 160

Ala Ala Ala Thr Arg Glu Gln Met Arg Lys Asp Lys Ile Ile Tyr Gly
165 170 175

Asp Ser Ile Ser Tyr Arg His Met Cys Arg Tyr Glu Ser Gly Phe Phe
180 185 190

Phe Lys His Pro Glu Leu Ala Glu Tyr Glu Tyr Tyr Trp Arg Val Glu
195 200 205

Pro Ser Ile Lys Ile Tyr Cys Asp Ile Asp Tyr Asp Ile Phe Lys Phe
210 215 220

Met Lys Asp Asn Lys Lys Ser Tyr Gly Trp Thr Ile Ser Leu Pro Glu
225 230 235 240

Tyr Lys Glu Thr Ile Pro Thr Leu Trp Lys Thr Thr Arg Asp Phe Met
245 250 255

Lys Glu Asn Pro Gln Tyr Val Ala Gln Asp Asn Leu Ile Asn Phe Ile
260 265 270

Ser Asp Asp Gly Gly Ser Ser Tyr Asn Gly Cys His Phe Trp Ser Asn
275 280 285

Phe Glu Val Gly Ser Leu Glu Phe Trp Arg Gly Glu Ala Tyr Thr Lys
290 295 300

Tyr Phe Glu Ala Leu Asp Gln Ala Gly Gly Phe Phe Tyr Glu Arg Trp
305 310 315 320

Gly Asp Ala Pro Ile His Ser Ile Ala Val Ala Leu Phe Met Pro Lys
325 330 335

Asp Glu Val His Phe Phe Asp Asp Val Gly Tyr Phe His Asn Pro Phe
340 345 350

His Asn Cys Pro Ile Asp Asn Ala Val Arg Glu Ala Lys Asn Cys Val
355 360 365

Cys Asn Gln Ala Asp Asp Phe Thr Phe Gln His Tyr Ser Cys Thr Pro
370 375 380

Lys Phe Tyr Gln Glu Met Gly Leu Lys Lys Pro Ala Asn Trp Glu Gln
385 390 395 400

Tyr Ile His

<210> 65

<211> 10

<212> PRT

<213> Saccharomyces cerevisiae

<400> 65

Thr Ser Trp Val Leu Trp Leu Asp Ala Asp

1 5 10

<210> 66

<211> 10

<212> PRT

<213> Saccharomyces cerevisiae

<400> 66

Glu Thr Glu Gly Phe Ala Lys Met Ala Lys

1 5 10

<210> 67

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PMN5 for amplification of 5'-region of Ogataea minuta MNN9 gene

<400> 67

acnwsntggg tnytntggyt ngaygcnga 29

<210> 68

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PMN3 for amplification of 3'-region of Ogataea minuta MNN9 gene

<400> 68

ttngccatyt tngcraancc ytcngtytc 29

<210> 69

<211> 2221

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 931..2034

<400> 69

gggcccagag gaggaggtag gagtgggggg atcgccaatt ttctggcgcg ctactccgcg 60

ctgccccgca cttcggccgc accgccaacc ttttctttgc gcacccccctc tccaacgttt 120

ccggcctttc cattgaagcg agctaagcag tcagagagca ccaccgggag acgtgatcgc 180

agcccctgtt tgccccgaaa ccgggttaga caaaacgcgg ttcggcttca acggactctc 240

atctttcaga tggccgcagg ttgctggcag cttcgggctg acaacatcat ggctgacgta 300
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t 2221

<210> 70
<211> 367
<212> PRT
<213> Ogataea minuta

<400> 70

Met Leu Lys Gly Val Leu Lys His Pro Leu Val His Gln Ile Arg Arg
1 5 10 15

Lys Pro Val Lys Val Leu Val Pro Val Phe Gly Leu Ala Val Leu Leu
20 25 30

Phe Leu Val Phe Gly Gly Ser Ser Ser Asn Arg Lys Thr Asn Ser Pro
35 40 45

Tyr Ser Tyr Lys Arg Asn Asn Arg Asp Glu Val Ile Pro Arg Asn Leu
50 55 60

Pro Ala Asp His Ile Ser His Tyr Asp Leu Asn Asn Leu Ala Ser Thr
65 70 75 80

Pro Met Ala Ala Tyr Asn Lys Glu Arg Val Leu Ile Leu Thr Pro Met
85 90 95

Ala Lys Phe Leu Asp Gly Tyr Trp Asp Asn Leu Leu Lys Leu Thr Tyr
100 105 110

Pro Arg Asp Leu Ile Glu Leu Gly Phe Ile Val Pro Arg Thr Ala Glu
115 120 125

Gly Asp Gln Ala Leu Lys Lys Leu Glu His Ala Val Lys Ile Ile Gln
130 135 140

Asn Pro Lys Asn Thr Lys Glu Pro Lys Phe Ala Lys Val Thr Ile Leu
145 150 155 160

Arg Gln Asp Asn Glu Ser Leu Ser Ser Gln Ser Glu Lys Asp Arg His
165 170 175

Ala Phe Lys Val Gln Lys Glu Arg Arg Ala Gln Met Ala Thr Ala Arg
180 185 190

Asn Ser Leu Leu Phe Thr Thr Ile Gly Pro Tyr Thr Ser Trp Val Leu
195 200 205

Trp Leu Asp Ser Asp Ile Val Glu Ser Pro His Thr Leu Ile Gln Asp
210 215 220

Leu Val Ser His Asp Lys Pro Val Ile Ala Ala Asn Cys Tyr Gln Arg
225 230 235 240

Tyr Tyr Asp Glu Asp Lys Lys Glu Asp Ser Ile Arg Pro Tyr Asp Phe

245 250 255

Asn Asn Trp Ile Glu Ser Glu Glu Gly Leu Arg Ile Ala Ser Thr Met
260 265 270

Ser Asp Asp Glu Ile Ile Val Glu Ala Tyr Ala Glu Ile Ala Thr Tyr
275 280 285

Arg Pro Leu Met Gly His Phe Tyr Asp Pro Asn Gly Asp Leu Gly Thr
290 295 300

Glu Met Gln Leu Asp Gly Val Gly Gly Thr Cys Leu Met Val Lys Ala
305 310 315 320

Asp Val His Arg Asp Gly Ala Met Phe Pro Asn Phe Pro Phe Tyr His
325 330 335

Leu Ile Glu Thr Glu Gly Phe Ala Lys Met Ala Lys Arg Leu Gly Tyr
340 345 350

Gln Val Phe Gly Leu Pro Asn Tyr Leu Val Phe His Tyr Asn Glu
355 360 365

<210> 71

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DMN5

<400> 71

agatgaggtg attccacgta atttgccagc 30

<210> 72

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DMN3

<400> 72

ttttgattgt catctatttc gcacaccctg 30

<210> 73

<211> 12

<212> PRT

<213> Pichia pastoris

<400> 73

Gly Gly Gly Ser Ser Ile Asn Phe Met Met Tyr Thr

1 5 10

<210> 74

<211> 10

<212> PRT

<213> Pichia pastoris

<400> 74

Asp Met Trp Pro Met Val Trp Ala Tyr Lys
1 5 10

<210> 75

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer PAX5 for amplification of 5'-region of Ogataea minuta AOX1 gene

<400> 75

ggnggnggnw snwsnathaa yttyatgatg tayac 35

<210> 76

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PAX3 for amplification of 3'-region of Ogataea minuta AOX1 gene

<400> 76

ttrtangccc anaccatngg ccacatrtc 29

<210> 77

<211> 5817

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 2349..4340

<400> 77

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aggcgcactt taaaagataa tctacatcca gaaaaataaa aaaataaaac tgaaccggca 120
tttgcgatta cgtaagccac aaaatttcag gaaactcgta caagatcagg ttggcgaggg 180
ggctagcgat agaatgtatc agtgttatta gtggctctag gagtagaaaa caatagaata 240
aagatccgaa gaaagggagc aagaaggcca cgccagacgt tctagtaggt agcccaatcg 300
tcaatgtagc tgttcaggtc tttcaacagg ttcttggtct cgtctggact ggagatccaa 360
caagtcgttg ctgcggttcg actggcatag tcgttggcgc cgagggagct gaactggtcg 420
ccgacgtgca gggtgttttc gggcttgatg gttcggttgt cgttgcagct gaggaactct 480
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<210> 78
<211> 663
<212> PRT
<213> Ogataea minuta

<400> 78
Met Ala Ile Pro Asp Glu Phe Asp Ile Ile Val Val Gly Gly Gly Ser
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Cys Gly Cys Ala Ile Ala Gly Arg Leu Gly Asn Leu Asp Pro Asp Val
20 25 30

Thr Val Ala Leu Ile Glu Gly Gly Glu Asn Asn Ile Asn Asn Pro Trp
35 40 45

Val Tyr Leu Pro Gly Val Tyr Pro Arg Asn Met Arg Leu Asp Ser Lys
50 55 60

Thr Ala Thr Phe Tyr Asn Ser Arg Pro Ser Lys His Leu Asn Gly Arg
65 70 75 80

Arg Ala Ile Val Pro Cys Ala Asn Ile Leu Gly Gly Gly Ser Ser Ile
85 90 95

Asn Phe Leu Met Tyr Thr Arg Ala Ser Ala Ser Asp Tyr Asp Asp Trp
100 105 110

Glu Gln Glu Gly Trp Thr Thr Asp Glu Leu Leu Pro Leu Met Lys Lys
115 120 125

Leu Glu Thr Tyr Gln Arg Pro Cys Asn Asn Arg Glu Val His Gly Phe
130 135 140

Asp Gly Pro Ile Lys Val Ser Phe Gly Asn Tyr Thr Tyr Pro Thr Ala
145 150 155 160

Gln Asp Phe Leu Arg Ala Cys Glu Ser Gln Gly Ile Pro Phe Asn Asp

165 170 175

Asp Leu Glu Asp Leu Lys Ala Ser His Gly Ala Glu Tyr Trp Leu Lys
180 185 190

Trp Ile Asn Arg Asp Leu Gly Arg Arg Ser Asp Ser Ala His Ala Tyr
195 200 205

Ile His Pro Thr Met Arg Asn Lys Ser Asn Leu Phe Leu Ile Thr Ser
210 215 220

Thr Lys Ala Asp Lys Val Ile Ile Glu Asn Gly Val Ala Val Gly Val
225 230 235 240

Arg Thr Val Pro Met Lys Pro Val Glu Thr Lys Asn Pro Pro Ser Arg
245 250 255

Ile Phe Lys Ala Arg Lys Gln Ile Val Val Ser Cys Gly Thr Ile Ser
260 265 270

Ser Pro Leu Val Leu Gln Arg Ser Gly Ile Gly Ala Ala His Lys Leu
275 280 285

Arg Gln Ala Gly Ile Lys Pro Ile Val Asp Leu Pro Gly Val Gly Glu
290 295 300

Asn Phe Gln Asp His Tyr Cys Phe Phe Thr Pro Tyr Tyr Ser Lys Pro
305 310 315 320

Glu Val Pro Thr Phe Asp Asp Phe Val Arg Gly Asp Pro Val Ala Gln
325 330 335

Lys Ser Ala Phe Asp Gln Trp Tyr Ser Asn Lys Asp Gly Pro Leu Thr
340 345 350

Thr Asn Gly Ile Glu Ala Gly Val Lys Ile Arg Pro Thr Asp Glu Glu
355 360 365

Leu Ala Thr Ala Asp Asp Asp Phe Ile Gln Gly Tyr His Glu Tyr Phe
370 375 380

Asp Asn Lys Pro Asp Lys Pro Leu Met His Tyr Ser Val Ile Ser Gly
385 390 395 400

Phe Phe Gly Asp His Thr Lys Ile Pro Asn Gly Lys Phe Phe Thr Met
405 410 415

Phe His Phe Leu Glu Tyr Pro Phe Ser Arg Gly Phe Val Tyr Ala Val
420 425 430

Ser Pro Asp Pro Tyr Glu Ala Pro Asp Phe Asp Pro Gly Phe Leu Asn
435 440 445

Asp Ser Arg Asp Met Trp Pro Met Val Trp Ser Tyr Lys Lys Ser Arg
450 455 460

Gln Thr Ala Arg Arg Met Glu Ser Phe Ala Gly Glu Val Thr Ser His
465 470 475 480

His Pro Leu Tyr Pro Val Asp Ser Pro Ala Arg Ala Lys Asp Leu Asp
485 490 495

Leu Glu Thr Cys Lys Ala Phe Ala Gly Pro Asn His Phe Thr Ala Asn
500 505 510

Leu Tyr His Gly Ser Trp Thr Val Pro Ile Glu Lys Pro Thr Pro Lys
515 520 525

Asn Asp Ser His Val Thr Cys Asn Gln Val Glu Ile Phe Ser Asp Ile
530 535 540

Asp Tyr Ser Ala Glu Asp Asp Glu Ala Ile Val Lys Tyr Ile Lys Glu
545 550 555 560

His Thr Glu Thr Thr Trp His Cys Leu Gly Thr Cys Ser Met Ala Pro
565 570 575

Gln Glu Gly Ser Lys Ile Ala Pro Lys Gly Gly Val Val Asp Ala Arg
580 585 590

Leu Asn Val Tyr Glu Val Lys Asn Leu Lys Val Ala Asp Leu Ser Ile
595 600 605

Cys Pro Asp Asn Val Gly Cys Asn Thr Tyr Ser Thr Ala Leu Leu Ile
610 615 620

Gly Glu Lys Ala Ala Thr Leu Val Ala Glu Asp Leu Gly Tyr Ser Gly

625 630 635 640

Ser Asp Leu Ala Met Thr Ile Pro Asn Phe Lys Leu Gly Thr Tyr Glu
645 650 655

Glu Lys Gly Leu Ala Arg Phe
660

<210> 79
<211> 2348
<212> DNA
<213> Ogataea minuta

<400> 79
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tttgcgatta cgtaagccac aaaatttcag gaaactcgta caagatcagg ttggcgaggg 180
ggctagcgat agaatgtatc agtgttatta gtggctctag gagtagaaaa caatagaata 240
aagatccgaa gaaagggagc aagaaggcca cgccagacgt tctagtaggt agcccaatcg 300
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ccgacgtgca gggtgttttc gggcttgatg gttcggttgt cgttgcagct gaggaactct 480
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aaactgcgta taaatagcta cttccatctc ctacttgttg caccattgcc atagtaagaa 2280
aagaagcaga tcactcaact tgttcaaaga ctcttgtgtt ctgttacgac ttacgactta 2340
cgaaaaaa 2348

<210> 80

<211> 802

<212> DNA

<213> Ogataea minuta

<400> 80

gagacggtgc ccgactcttg ttcaattctt ttggttcttt ttctgttttt ctctacgatt 60
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atcgacaatt acgactcgtt cacatggaac ttgtacgagt atctttgtca agagggagcc 420
gatgtcgagg tctatcgtaa cgacaagatc acaattgaag aaatcgagga aatgaagcct 480
gacattatag tgatttcgcc aggccccgga catccgagat cggactctgg tatctctcga 540
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tgcatttacg aggttttcgg gggagacgtt gagtacgctg gtgaaattgt tcacggaaaa 660
acctcttctg tgacccacga caatcgtgga gtcttcaaga acgttccgca gggagttgct 720
gtgacgagat accattcgtt ggctggaacg ctaaaaactt tgcccagcga gttggaggtg 780
actgcccgta ccactaacgg ta 802

<210> 81

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer OAP5 for production of an expression cassette with AOX1 gene promoter and terminator

<400> 81

ctgcagcccc ttctgttttt cttttgacgg 30

<210> 82

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer OAP3 for production of an expression cassette with AOX1 gene promoter and terminator

<400> 82

cccccggatc caggaacccg ggaacagaat ctagattttt tcgtaagtcg taagtcgtaa 60

cagaacacaa gagtctttga acaagttgag 90

<210> 83

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer OAT5 for production of an expression cassette with AOX1 gene promoter and terminator

<400> 83

ccccccccgga tccgagacgg tgcccgactc ttgttcaatt cttttgg 47

<210> 84

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer OAT3 for production of an expression cassette with AOX1 gene promoter and terminator

<400> 84

cccataatgg taccgttagt ggtacgggca gtc 33

<210> 85

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer HGP5 for amplification of a gene conferring resistance against hygromycin B

<400> 85

gtcgacatga aaaagcctga actcaccgc 29

<210> 86

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer HGP3 for amplification of a gene conferring resistance against hygromycin B

<400> 86

actagtctat tcctttgccc tcggacg 27

<210> 87

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of 5'-region of α-mannosidase gene

<400> 87

gggggtcga catggtggtc ttcagcaaaa ccgctgccc 39

<210> 88

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of 5'-region of α-mannosidase gene

<400> 88

gggggcggc cgcgtgatgt tgaggttgtt gtacggaacc ccc 43

<210> 89

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of Saccharomyces cerevisiae SUC2 gene

<400> 89

ggggactagt atgcttttgc aagctttcct tttccttttg 40

<210> 90

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of Saccharomyces cerevisiae SUC2 gene

<400> 90

ccccagatct tattttactt cccttacttg gaacttgtc 39

<210> 91

<211> 711

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 7..711

<400> 91

ctcaccatga gggtccccgc tcagctcctg gggctcctgc tgctctggct cccaggtgca 60
cgatgtgaca tccagatgac ccagtctcca tcttccgtgt ctgcatctgt aggagacaga 120
gtcaccatca cttgtcgggc gagtcaggtt attagcagct ggttagcctg gtatcagcag 180
aaaccaggga aagcccctaa gctcctgatc tatgctgcat ccagtttgca aagtggggtc 240
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ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
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ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgttg a 711

<210> 92

<211> 234

<212> PRT

<213> Homo sapiens

<400> 92

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val
35 40 45

Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn
100 105 110

Ser Phe Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 93
<211> 1428
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..1428

<400> 93
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<213> Homo sapiens

<400> 94
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Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

35 40 45

Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Asp Arg Ile Ile Met Val Arg Gly Val Tyr Tyr
115 120 125

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
130 135 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
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Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
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Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
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Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
195 200 205

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210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
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Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
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Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
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Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
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Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
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Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
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Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
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Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
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Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
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<212> PRT

<213> Saccharomyces cerevisiae

<400> 95

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<210> 96

<211> 7

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<213> Saccharomyces cerevisiae

<400> 96

Pro Ser Thr Lys Gly Val Leu

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<210> 97

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PHI5 for amplification of Ogataea minuta HIS3 gene

<400> 97

tnggnttyyt ngaycayatg 20

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PHI3 for amplification of Ogataea minuta HIS3 gene

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<210> 99

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<212> DNA

<213> Ogataea minuta

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<221> CDS

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<211> 238

<212> PRT

<213> Ogataea minuta

<400> 100

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35 40 45

Glu Ser Ile Leu Gly Ala Thr Tyr Glu Lys Glu Ser His Ala Ala Gln
50 55 60

Asn Thr Ser Ala Gln Val Ile Ser Ile Lys Thr Gly Leu Gly Phe Leu
65 70 75 80

Asp His Met Leu His Ala Leu Ala Lys His Ser Gly Trp Ser Leu Ile
85 90 95

Val Glu Cys Ile Gly Asp Leu His Ile Asp Asp His His Thr Ala Glu
100 105 110

Asp Val Gly Ile Ala Leu Gly Glu Thr Phe Lys Arg Ala Leu Gly Pro
115 120 125

Val Lys Gly Leu Lys Arg Phe Gly His Ala Tyr Ala Pro Leu Asp Glu
130 135 140

Ala Leu Ser Arg Ala Val Val Asp Leu Ser Asn Arg Pro Phe Ala Val
145 150 155 160

Val Glu Leu Gly Leu Arg Arg Glu Lys Ile Gly Asp Leu Ser Cys Glu
165 170 175

Met Ile Pro His Val Leu Glu Ser Phe Ala Thr Ser Ala His Ile Thr
180 185 190

Met His Val Asp Cys Leu Arg Gly Phe Asn Asp His His Arg Ser Glu
195 200 205

Ser Ala Phe Lys Ala Leu Ala Val Ala Ile Arg Asp Ala Thr Ser Tyr
210 215 220

Thr Gly Arg Asp Asp Val Pro Ser Thr Lys Gly Val Leu Met
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer DHI5

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<210> 102

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DHI3

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<210> 103

<211> 8

<212> PRT

<213> Saccharomyces cerevisiae

<400> 103

Ala Val Gly Gly Pro Lys Trp Gly

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<210> 104

<211> 7

<212> PRT

<213> Saccharomyces cerevisiae

<400> 104

Ala Ala Met Met Leu Lys Leu

1 5

<210> 105

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PLE5 for amplification of Ogataea minuta LEU2 gene

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gcngtnggng gnccnaartg ggg 23

<210> 106

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PLE3 for amplification of Ogataea minuta LEU2 gene

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<212> DNA

<213> Ogataea minuta

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<221> CDS

<222> 1606..2694

<400> 107

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<210> 108
<211> 363
<212> PRT
<213> Ogataea minuta

<400> 108
Met Thr Thr Lys Asn Ile Val Leu Leu Pro Gly Asp His Val Gly Pro
1 5 10 15

Glu Val Val Asp Glu Ala Val Lys Val Leu Asn Ala Ile Ser Ala Ala
20 25 30

Lys Pro Glu Ile Lys Phe Asn Phe Glu His His Leu Ile Gly Gly Ala
35 40 45

Ala Ile Asp Ala Thr Gly Gln Pro Ile Thr Asp Ala Ala Leu Glu Ala
50 55 60

Ser Lys Lys Ala Asp Ala Val Leu Leu Gly Ser Val Gly Gly Pro Lys
65 70 75 80

Trp Gly Thr Gly Gln Val Arg Pro Glu Gln Gly Leu Leu Lys Ile Arg
85 90 95

Lys Glu Leu Asn Leu Tyr Ala Asn Leu Arg Pro Cys Ser Phe Ala Ser
100 105 110

Asp Ala Leu Leu Asp Leu Ser Pro Leu Lys Pro Glu Ile Val Arg Gly
115 120 125

Thr Asp Phe Val Val Val Arg Glu Leu Val Gly Gly Ile Tyr Phe Gly
130 135 140

Glu Arg Lys Glu Asp Asp Gly Ser Gly Phe Ala Ser Asp Thr Glu Ala
145 150 155 160

Tyr Ser Val Pro Glu Val Gln Arg Ile Thr Arg Met Ala Ala Phe Met
165 170 175

Ala Leu Gln Ser Asp Pro Pro Leu Pro Val Tyr Ser Leu Asp Lys Ala
180 185 190

Asn Val Leu Ala Ser Ser Arg Leu Trp Arg Lys Thr Val Glu Glu Thr
195 200 205

Ile Lys Asn Glu Phe Pro Gln Leu Lys Leu Gln His His Leu Ile Asp
210 215 220

Ser Ala Ala Met Ile Leu Val Lys Ser Pro Thr Lys Leu Asn Gly Val
225 230 235 240

Val Leu Thr Ser Asn Met Phe Gly Asp Ile Ile Ser Asp Glu Ala Ser
245 250 255

Val Ile Pro Gly Ser Leu Gly Leu Leu Pro Ser Ala Ser Leu Ala Ser
260 265 270

Leu Pro Asp Ser Asn Glu Ala Phe Gly Leu Tyr Glu Pro Cys His Gly
275 280 285

Ser Ala Pro Asp Leu Ala Lys Gly Leu Val Asn Pro Leu Ala Thr Ile
290 295 300

Leu Ser Ala Ala Met Met Leu Lys Leu Ser Leu Asn Leu Val Glu Glu
305 310 315 320

Gly Arg Ala Val Glu Lys Ala Val Arg Ala Val Leu Asp Gln Gly Ile
325 330 335

Met Thr Ala Asp Leu Gly Gly Ser Ser Ser Thr Thr Glu Val Gly Asp
340 345 350

Ala Val Ala Lys Glu Val Thr Lys Leu Leu Gly

355 360

<210> 109

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DL5

<400> 109

caggagctac agagtcatcg 20

<210> 110

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DL3

<400> 110

acgagggaca ggttgctcgc 20

<210> 111

<211> 8

<212> PRT

<213> Saccharomyces cerevisiae

<400> 111

Asp Thr Gly Ser Ser Asp Leu Trp

1 5

<210> 112

<211> 8

<212> PRT

<213> Saccharomyces cerevisiae

<400> 112

Phe Gly Ala Ile Asp His Ala Lys

1 5

<210> 113

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PLE5 for amplification of Ogataea minuta YPS1 gene

<400> 113

gayacngght cntcngayyt ntgg 24

<210> 114

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PLE3 for amplification of Ogataea minuta YPS1 gene

<400> 114

ttygghgcna tygaycaygc naa 23

<210> 115

<211> 3661

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 1712..3523

<400> 115

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ccgcctatag ttctgggttg ccatcacatc atatcgaagg agagcgctga caagctattg 360

aaacagattt tccgggtgaa gtgtccatac tgtccaatga cttggtatga agatcgtctc 420

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c 3661

<210> 116
<211> 604
<212> PRT
<213> Ogataea minuta

<400> 116

Met Leu Leu Val Ala Gly Gly Thr Val Pro Val Ala Gly Leu Pro Ala
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Gly Glu Ser Lys Ala Asn Ser Ser Pro Gly Tyr Leu Arg Met Glu Ala
20 25 30

Glu Ile Tyr Arg Gly His Ser Phe Glu Thr Ser Gln Arg Gly Gly Arg
35 40 45

Pro Tyr Met Leu Glu Lys Arg Ala Glu Asp Gly Ser Val Leu Met Glu
50 55 60

Leu Gln Asn Asn Gln Ser Phe Tyr Lys Val Glu Leu Glu Val Gly Ser
65 70 75 80

Asp Lys Gln Lys Ile Gly Val Leu Val Asp Thr Gly Ser Ser Asp Leu
85 90 95

Trp Ile Met Asn Gln Asn Asn Ser Tyr Cys Glu Ser Ser Ser Ser Ser
100 105 110

Ser Lys Met Arg Glu Arg Lys Gly Arg Lys Leu Ser Asp Leu Arg Asn
115 120 125

Leu Asn Leu Asp Val Ser Glu Lys Asn Val Lys Ala Val Gly Ala Ala
130 135 140

Glu Thr Glu Thr Met Thr Leu Ser Val Gly Glu Gly Leu Phe Ser Trp
145 150 155 160

Phe Glu Thr Gln Thr Asp Gly Ser Gly Gly Glu Thr Glu Thr Ala Ser
165 170 175

Gly Asp Ser Ser Glu Ala Thr Ile Asp Cys Ser Val Tyr Gly Thr Phe
180 185 190

Asp Pro Ser Ser Ser Asp Thr Phe Lys Ser Asn Gly Thr Glu Phe Ser
195 200 205

Ile Ser Tyr Ala Asp Asp Ser Phe Ala Lys Gly Thr Trp Gly Thr Asp
210 215 220

Asp Val Thr Phe Asn Gly Val Thr Val Asp Gln Leu Ser Met Ala Ile
225 230 235 240

Ala Asp Glu Thr Asn Ser Ser Met Gly Val Leu Gly Ile Gly Leu Lys
245 250 255

Gly Leu Glu Thr Thr Tyr Ser Gly Asp Val Thr Asn Ala Tyr Thr Tyr
260 265 270

Glu Asn Leu Pro Tyr Lys Met Gln Ser Gln Gly Leu Ile Ser Lys Pro
275 280 285

Val Tyr Ser Val Tyr Leu Asn Asp Ser Glu Ser Ser Ala Ala Ser Ile
290 295 300

Leu Phe Gly Ala Val Asp His Asp Lys Tyr Thr Gly Thr Leu Thr Leu

305 310 315 320

Leu Pro Ile Ile Asn Thr Ala Glu Ser Leu Gly Tyr Ser Thr Pro Val
325 330 335

Arg Leu Glu Val Thr Leu Ser Lys Leu Tyr Thr Gly Ser Ser Ser Asn
340 345 350

Lys Thr Ala Val Ser Ile Ala Ser Gly Ala Ala Ala Ala Leu Leu Asp
355 360 365

Thr Gly Thr Thr Leu Thr Tyr Val Pro Ser Asp Ile Ile Ser Thr Ile
370 375 380

Val Asp Gln Tyr Gly Phe Gln Tyr Ser Ser Ser Val Gly Thr Tyr Val
385 390 395 400

Ala Lys Cys Asp Ser Leu Asp Asp Ala Glu Ile Val Phe Asp Phe Gln
405 410 415

Gly Thr Lys Ile Trp Val Pro Phe Ser Ser Phe Ala Val Ser Leu Thr
420 425 430

Thr Asn Gly Gly Ser Gln Ser Ser Tyr Cys Ala Leu Gly Leu Met Asp
435 440 445

Ser Gly Asp Asp Thr Phe Thr Leu Gly Asp Ser Phe Leu Asn Asn Val
450 455 460

Tyr Phe Val Ala Asp Leu Glu Asn Leu Gln Ile Ala Ile Ala Pro Ala
465 470 475 480

Asn Leu Asp Ser Thr Ser Glu Asp Ile Glu Val Val Ser Asp Ser Gly
485 490 495

Ile Pro Ser Ala Lys Ser Ala Ser Ala Tyr Ser Ser Ser Trp Gly Ala
500 505 510

Ser Gly Ser Ala Val Ala Ser Ser Leu Ser Val Gln Thr Gly Ala Glu
515 520 525

Thr Val Thr Ser Thr Asp Ala Gly Ser Asp Ser Thr Gly Ser Ala Ser
530 535 540

Gly Ser Ser Gly Ser Ala Ser Ser Ser Ser Ser Lys Ser Ser Ala Ser
545 550 555 560

Ser Ser Ser Gly Ser Ser Gly Ser Ser Ser Lys Ser Gly Ser Ser Ser
565 570 575

Ser Lys Tyr Ala Ala Gly Asn Ala Trp Gly Met Ser Val Cys Ser Leu
580 585 590

Ala Phe Thr Ile Ala Val Ser Val Leu Val Ile Gly
595 600

<210> 117

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DY5

<400> 117

ctcaagggcc tggagactac g 21

<210> 118

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DY3

<400> 118

cgggattccc gagtcgctca cc 22

<210> 119

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PDI5 for amplification of 5'-region of Saccharomyces cerevisiae PDI gene

<400> 119

tctagaatga agttttctgc tggtgccgtc ctg 33

<210> 120

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PDI3 for amplification of 3'-region of Saccharomyces cerevisiae PDI gene

<400> 120

ggatccttac aattcatcgt gaatggcatc ttc 33